

80520

119

STIC-Biotech/ChemLib

187945

From: Bowman, Amy
Sent: Monday, May 01, 2006 5:09 AM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: sequence search-SEQ ID 82

Hello,
I need a search of SEQ ID NO: 82 in application 10/605,498, length limited to 35 nucleotides.
I need to include an interference search.

Thank you,
Amy Bowman
AU 1635
REM 2C31
mail REM 2C18
571-272-0755

BEST AVAILABLE COPY

Searcher: Jan
Searcher Phone: 122504
Date Searcher Picked up: 518104
Date completed: 518106
Searcher Prep Time: 10
Online Time: 15

Type of Search
NA# ✓ AA#:
S/L: Oligomer:
Encode/Transl:
Structure #: Text:
Inventor: Litigation:

Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM: ✓
WWW/Internet:
Other (Specify):

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4	16	80.0	21	6	CQ799905	Sequence
5	15	75.0	21	6	CQ799906	Sequence
6	14.2	71.0	33	6	AR559501	Sequence
7	14.2	71.0	33	6	AX473165	Sequence
8	13.2	66.0	27	6	E41696	Process for
9	13	65.0	20	6	AR454276	Sequence
10	12.8	64.0	23	6	BD243529	Nucleotide
11	12.8	64.0	23	6	AX034952	Sequence
12	12.8	64.0	24	6	AX684030	Sequence
13	12.6	63.0	24	6	BD081436	Productio
14	12.6	63.0	24	6	AR429338	Sequence
15	12.6	63.0	24	6	AR579704	Sequence
16	12.6	63.0	24	6	AR628409	Sequence
17	12.6	63.0	30	6	AR229807	Sequence
18	12.6	63.0	30	6	AR363940	Sequence

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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homnidae; Homo.
1
REFERENCE
AUTHORS Gleave,M.E., Rocchi,P. and Signaevsky,M.
TITLE Compositions for treatment of prostate and other cancers
JOURNAL Patent: WO 2004030660-A 81 15-APR-2004;
The University of British Columbia (CA)
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/db_xref="taxon:9606"
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DEFINITION Sequence 90 from Patent WO2004030660.
ACCESSION CQ799992
VERSION CQ799992.1 GI:46848939
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
REFERENCE
AUTHORS Gleave,M.E., Rocchi,P. and Signaevsky,M.
TITLE Compositions for treatment of prostate and other cancers
JOURNAL Patent: WO 2004030660-A 90 15-APR-2004;
The University of British Columbia (CA)
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ACCESSION CQ799905
VERSION CQ799905.1 GI:46848952
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
REFERENCE
AUTHORS Gleave,M.E., Rocchi,P. and Signaevsky,M.
TITLE Compositions for treatment of prostate and other cancers
JOURNAL Patent: WO 2004030660-A 3 15-APR-2004;
The University of British Columbia (CA)
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ACCESSION CQ799906
VERSION CQ799906.1 GI:46848853
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
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REFERENCE
AUTHORS Gleave,M.E., Rocchi,P. and Signaevsky,M.
TITLE Compositions for treatment of prostate and other cancers
JOURNAL Patent: WO 2004030660-A 4 15-APR-2004;
The University of British Columbia (CA)
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DEFINITION Sequence 16 from patent US 6750042.
ACCESSION AR559501
VERSION AR559501.1 GI:53968947
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Summers,A.O. and Caguiat,J.J.
TITLE Metal binding proteins, recombinant host cells and methods
JOURNAL Patent: US 6750042-A 16 15-JUN-2004;
University of Georgia Research Foundation, Inc.; Athens, GA
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 Db 19 GCACGAGGCGCTCGGATAT 1

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 DEFINITION Sequence 14 from patent US 6784346.
 ACCESSION AR579704
 VERSION AR579704.1 GI:56583159
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 24)
 AUTHORS Cho, W.-J., Lemaux, P.G., Buchanan, B.B., Wong, J. and Marx, C.
 TITLE Value-added traits in grain and seed transformed with thioredoxin
 JOURNAL Patent: US 6784346-A 14 31-AUG-2004;
 The Regents of the University of California; Oakland, CA
 FEATURES Location/Qualifiers
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 Db 19 GCACGAGGCGCTCGGATAT 1

Search completed: May 8, 2006, 09:47:45
 Job time : 1776 secs

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2006, 09:56:51 ; Search time 602 Seconds
(without alignments)
274.730 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 10726526

Minimum DB seq length: 0
Maximum DB seq length: 35

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_Main:*

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- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	15	75.0	21	7	US-10-605-498-4
7	14.2	71.0	25	10	US-11-036-317-261850
8	14.2	71.0	25	10	US-11-036-317-269817
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11	14.2	71.0	25	10	US-11-036-317-364465
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15	14.2	71.0	33	3	US-09-377-137A-16
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17	14	70.0	25	9	US-10-809-189-42173
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20	13.8	69.0	25	9	US-10-809-189-46325
21	13.6	68.0	25	7	US-10-719-956-135322
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24	13.6	68.0	25	10	US-11-036-317-912027	Sequence 912027,
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27	13.2	66.0	25	5	US-10-098-263B-65789	Sequence 65789, A
28	13.2	66.0	25	7	US-10-719-956-110491	Sequence 110491,
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c 30	13.2	66.0	25	7	US-10-719-956-547823	Sequence 547823,
31	13.2	66.0	25	8	US-10-719-900-148603	Sequence 148603,
32	13.2	66.0	25	8	US-10-719-900-849503	Sequence 849503,
33	13.2	66.0	25	8	US-10-719-900-849504	Sequence 849504,
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36	13.2	66.0	25	10	US-11-036-317-787134	Sequence 787134,
c 37	13.2	66.0	25	10	US-11-060-756-166335	Sequence 166335,
c 38	13.2	66.0	25	10	US-11-060-756-166384	Sequence 166384,
c 39	13.2	66.0	25	10	US-11-060-756-229339	Sequence 229339,
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41	13	65.0	20	5	US-10-206-654-19	Sequence 19, Appl
42	13	65.0	25	7	US-10-719-956-632447	Sequence 632447,
43	13	65.0	25	10	US-11-036-317-883329	Sequence 883329,
44	13	65.0	25	10	US-11-036-317-937963	Sequence 937963,
45	12.8	64.0	24	5	US-10-193-692-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-605-498-82
; Sequence 82, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; FILE REFERENCE: UBC.P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-498-82

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Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCTAT 20
Db 1 GGGACGCGCGCTCGGTCTAT 20

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US-10-605-498-81
; Sequence 81, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; FILE REFERENCE: UBC.P-031
; CURRENT APPLICATION NUMBER: US/10/605,498

; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-498-81

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US-10-605-498-90/c
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; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; FILE REFERENCE: UBC.P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
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; SEQ ID NO 90
; TYPE: RNA
; ORGANISM: Homo sapiens
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; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; FILE REFERENCE: UBC.P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18

; NUMBER OF SEQ ID NOS: 91
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; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
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; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 135321
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-135321

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; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; FILE REFERENCE: UBC.P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-498-4

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 7 GGGACGGCGGCTCG 21
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RESULT 7

US-11-036-317-261850
; Sequence 261850, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 261850
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-261850

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Best Local Similarity 84.2%; Pred. No. 3.6e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 3 GGGACGGCGGCTCGGTCA 21
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; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 269817
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-269817

Query Match 71.0%; Score 14.2; DB 10; Length 25;

Best Local Similarity 84.2%; Pred. No. 3.6e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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|||||

Db 5 GGGACGGCGGCTCGGTCA 23
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US-11-036-317-330516
; Sequence 330516, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan

; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
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; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-330516

Query Match 71.0%; Score 14.2; DB 10; Length 25;

Best Local Similarity 84.2%; Pred. No. 3.6e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCA 19
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Db 1 GGGACGGCGGCTCGGTCA 19
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RESULT 10

US-11-036-317-332488
; Sequence 332488, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
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; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-332488

Query Match 71.0%; Score 14.2; DB 10; Length 25;

Best Local Similarity 84.2%; Pred. No. 3.6e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCA 19
|||||

Db 2 GGGACGGCGGCTCGGTCA 20
|||||

RESULT 11

US-11-036-317-364465
; Sequence 364465, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 364465
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-364465

US-11-036-317-364465

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCA 19
|||||
Db 4 GGGACGCGCGATCTGCCA 22

RESULT 12

US-11-036-317-406575
; Sequence 406575, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 406575
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-406575

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCA 19
|||||
Db 7 GGGACGAGCGCTTTGTCA 25

RESULT 13

US-11-036-317-536426
; Sequence 536426, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 536426
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-536426

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCA 19
|||||
Db 7 GGGACGAGCGCTTTGTCA 25

RESULT 14

US-11-036-317-536427

; Sequence 536427, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 536427
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-536427

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCA 19
|||||
Db 7 GGGACGTGCGCTTTGTCA 25

RESULT 15

US-09-977-137A-16
; Sequence 16, Application US/09977137A
; Publication No. US20030104524A1
; GENERAL INFORMATION:
; APPLICANT: Summers, Anne O.
; TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 79-00
; CURRENT APPLICATION NUMBER: US/09/977,137A
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,465
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-977-137A-16

Query Match 71.0%; Score 14.2; DB 3; Length 33;
Best Local Similarity 84.2%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCA 19
|||||
Db 6 GGGTCTCGCGCTCGGCA 24

Search completed: May 8, 2006, 10:41:19
JOB time : 602 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2006, 09:12:57 ; Search time 279 Seconds
(without alignments)
477.756 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20
Sequence: 1 gggacgcggcgctcggtcat 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 4393292

Minimum DB seq length: 0
Maximum DB seq length: 35

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21.*
1: geneseqn1980s.*
2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002as.*
7: geneseqn2002bs.*
8: geneseqn2003as.*
9: geneseqn2003bs.*
10: geneseqn2003cs.*
11: geneseqn2003ds.*
12: geneseqn2004as.*
13: geneseqn2004bs.*
14: geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20	100.0	20	12 ADM94732	Adm94732 Human hea
2	20	100.0	21	12 ADM94731	Adm94731 Human hea
3	19	95.0	19	12 ADM94740	Adm94740 Human hea
4	16	80.0	21	12 ADM94653	Adm94653 Human hea
5	15	75.0	21	12 ADM94654	Adm94654 Human hea
6	14.2	71.0	33	6 ABK52211	ABK52211 Synthetic
7	14	70.0	25	9 ACH58106	ACH58106 Human mic
8	13.2	66.0	25	9 ACI03862	ACI03862 Human mic
9	13.2	66.0	25	9 ACI65798	ACI65798 Human mic
10	13.2	66.0	27	4 AAH21740	AAH21740 Corynebac
11	12.8	64.0	21	2 AAU51704	AAU51704 Zea mays
12	12.8	64.0	23	3 AAA75395	AAA75395 Fragment
13	12.8	64.0	24	8 ABZ58873	ABZ58873 Zebrafish
14	12.8	64.0	25	9 ACI84537	ACI84537 Human mic
15	12.8	64.0	29	12 ADO31537	ADO31537 Human CFT
16	12.8	64.0	30	14 ADY40845	ADY40845 PCR fragm
17	12.6	63.0	20	6 ABZ08781	ABZ08781 Human CMV
18	12.6	63.0	22	10 ACD26306	ACD26306 Bar assoc
19	12.6	63.0	24	2 AAX34633	AAX34633 Bar gene

C 20	12.6	63.0	24	3 AAC61525	Aac61525 PCR prime
C 21	12.6	63.0	24	3 AAC62482	Aac62482 Wheat thi
C 22	12.6	63.0	24	10 AAD59639	Aad59639 Bar ampli
C 23	12.6	63.0	25	13 ADS86174	Ads86174 PCAV-deci
C 24	12.6	63.0	29	4 ABU96187	Abu96187 Primer #3
C 25	12.6	63.0	30	2 AAV44737	Aav44737 Fluoresce
C 26	12.6	63.0	31	2 AAT38854	Aat38854 Primer fo
C 27	12.6	63.0	31	12 ADO05568	Ado05568 Plasmid R
C 28	12.6	63.0	33	14 AEA35882	Aea35882 Mouse mid
C 29	12.4	62.0	19	3 AAA40594	Aaa40594 Human Arp
C 30	12.4	62.0	20	2 AAQ36810	Aaq36810 Oligomer
C 31	12.4	62.0	20	2 AAQ94968	Aaq94968 PCR prime
C 32	12.4	62.0	20	2 AAV35805	Aav35805 PCR prime
C 33	12.4	62.0	20	2 AAV99501	Aav99501 Plasmid p
C 34	12.4	62.0	20	8 ADA16031	Ada16031 Plasmid p
C 35	12.4	62.0	20	9 ACH03677	Ach03677 Plasmid p
C 36	12.4	62.0	20	10 ADF73001	Adf73001 Probe rel
C 37	12.4	62.0	20	14 ADW71639	Adw71639 Plasmid p
C 38	12.4	62.0	24	6 ABQ07627	Abq07627 Oligonuc1
C 39	12.4	62.0	24	6 ABQ01856	Abq01856 Oligonuc1
C 40	12.4	62.0	24	6 ABQ07668	Abq07668 Oligonuc1
C 41	12.4	62.0	24	12 ADO38198	Ado38198 HIV envel
C 42	12.4	62.0	24	12 ADO38213	Ado38213 HIV envel
C 43	12.4	62.0	24	12 ADO38185	Ado38185 HIV envel
C 44	12.4	62.0	24	12 ADO38102	Ado38102 HIV envel
C 45	12.4	62.0	24	12 ADO38074	Ado38074 HIV envel

ALIGNMENTS

RESULT 1

ADM94732

ID ADM94732 standard; DNA; 20 BP.

XX AC ADM94732;

XX DT 01-JUL-2004 (first entry)

XX DE Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:82.

XX KW heat shock protein 27; hsp27; cytostatic; gene therapy;

XX KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;

XX KW antisense oligonucleotide; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO2004030660-A2.

XX PD 15-APR-2004.

XX PF 02-OCT-2003; 2003WO-CA001588.

XX PR 02-OCT-2003; 2002US-0415859P.

XX PR 18-APR-2003; 2003US-0463952P.

XX PA (UYBR-) UNIV BRITISH COLUMBIA.

XX PI Gleave ME, Rocchi P, Signaevsky M;

XX PI WPI; 2004-316331/29.

XX PT New composition comprising a therapeutic agent that reduces the amount of

XX PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,

XX PT useful in treating cancer, e.g., prostate cancer or a central nervous

XX PT system malignancy.

XX PS Claim 6; SEQ ID NO 82; 38pp; English.

XX CC The present invention describes a composition which comprises a

XX CC therapeutic agent that reduces the amount of active heat shock protein 27

XX CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The

CC composition has cytostatic activity, and can be used in gene therapy. The
CC composition is useful in treating cancer, e.g., prostate, bladder, lung,
CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
CC cancer or a central nervous system malignancy. The present sequence
CC represents a human hsp27 antisense oligonucleotide which is used in the
CC exemplification of the present invention.

SQ Sequence 20 BP; 2 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCAAT 20
DB 1 GGGACGGCGGCTCGGTCAAT 20
|||||

RESULT 2

ADM94731
ID ADM94731 standard; DNA; 21 BP.

AC ADM94731;

XX 01-JUL-2004 (first entry)

DE Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:81.

XX heat shock protein 27; hsp27; cytostatic; gene therapy;

KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;

KW antisense oligonucleotide; as.

XX Homo sapiens.

OS Synthetic.

XX WO2004030660-A2.

XX 15-APR-2004.

XX 02-OCT-2003; 2003WO-CA001588.

XX 02-OCT-2002; 2002US-0415859P.

PR 18-APR-2003; 2003US-0463952P.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Gleave ME, Rocchi P, Signaevsky M;

XX WPI; 2004-316331/29.

XX New composition comprising a therapeutic agent that reduces the amount of
PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
PT useful in treating cancer, e.g., prostate cancer or a central nervous
PT system malignancy.

XX Claim 5; SEQ ID NO 81; 38pp; English.

XX The present invention describes a composition which comprises a
CC therapeutic agent that reduces the amount of active heat shock protein 27
CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The
CC composition has cytostatic activity, and can be used in gene therapy. The
CC composition is useful in treating cancer, e.g., prostate, bladder, lung,
CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
CC cancer or a central nervous system malignancy. The present sequence
CC represents a human hsp27 antisense oligonucleotide which is used in the
CC exemplification of the present invention.

SQ Sequence 21 BP; 2 A; 6 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCAAT 20
DB 2 GGGACGGCGGCTCGGTCAAT 21
|||||

RESULT 3

ADM94740/c

ID ADM94740 standard; DNA; 19 BP.

XX ADM94740;

XX 01-JUL-2004 (first entry)

DE Human heat shock protein 27 siRNA oligonucleotide SEQ ID NO:90.

XX heat shock protein 27; hsp27; cytostatic; gene therapy;

KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;

KW short interfering RNA; siRNA; RNA interference; RNAi; ds.

XX Homo sapiens.

OS Synthetic.

XX WO2004030660-A2.

XX 15-APR-2004.

XX 02-OCT-2003; 2003WO-CA001588.

XX 02-OCT-2002; 2002US-0415859P.

PR 18-APR-2003; 2003US-0463952P.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Gleave ME, Rocchi P, Signaevsky M;

XX WPI; 2004-316331/29.

XX New composition comprising a therapeutic agent that reduces the amount of
PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
PT useful in treating cancer, e.g., prostate cancer or a central nervous
PT system malignancy.

XX Claim 10; SEQ ID NO 90; 38pp; English.

XX The present invention describes a composition which comprises a
CC therapeutic agent that reduces the amount of active heat shock protein 27
CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The
CC composition has cytostatic activity, and can be used in gene therapy. The
CC composition is useful in treating cancer, e.g., prostate, bladder, lung,
CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
CC cancer or a central nervous system malignancy. The present sequence
CC represents a human hsp27 short interfering RNA (siRNA) oligonucleotide
CC which is used in the exemplification of the present invention.

XX Sequence 19 BP; 3 A; 8 C; 6 G; 0 T; 2 U; 0 Other;

Query Match 95.0%; Score 19; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACGGCGGCTCGGTCAAT 20
DB 19 GGACGGCGGCTCGGTCAAT 1
|||||

RESULT 4

ADM94653

ID ADM94653 standard; DNA; 21 BP.

XX ADM94653;

XX 01-JUL-2004 (first entry)

```
DE Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:3.
XX heat shock protein 27; hsp27; cytostatic; gene therapy;
KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
KW antisense oligonucleotide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX WO2004030660-A2.
XX
XX 15-APR-2004.
XX
XX 02-OCT-2003; 2003WO-CA001588.
XX
XX 02-OCT-2002; 2002US-0415859P.
XX
XX 18-APR-2003; 2003US-0463952P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Gleave ME, Rocchi P, Signaevsky M;
XX WPI; 2004-316331/29.
XX
XX New composition comprising a therapeutic agent that reduces the amount of
PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
PT useful in treating cancer, e.g., prostate cancer or a central nervous
PT system malignancy.
XX
XX Claim 5; SEQ ID NO 3; 38pp; English.
XX
XX The present invention describes a composition which comprises a
CC therapeutic agent that reduces the amount of active heat shock protein 27
CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The
CC composition has cytostatic activity, and can be used in gene therapy. The
CC composition is useful in treating cancer, e.g., prostate, bladder, lung,
CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
CC cancer or a central nervous system malignancy. The present sequence
CC represents a human hsp27 antisense oligonucleotide which is used in the
CC exemplification of the present invention.
XX
XX Sequence 21 BP; 1 A; 7 C; 9 G; 4 T; 0 U; 0 Other;
XX
XX The present invention describes a composition which comprises a
CC therapeutic agent that reduces the amount of active heat shock protein 27
CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The
CC composition has cytostatic activity, and can be used in gene therapy. The
CC composition is useful in treating cancer, e.g., prostate, bladder, lung,
CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
CC cancer or a central nervous system malignancy. The present sequence
CC represents a human hsp27 antisense oligonucleotide which is used in the
CC exemplification of the present invention.
XX
XX Query Match 80.0%; Score 16; DB 12; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 8.2e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 5 CGCGCGCTCGGTCTAT 20
DB 1 CGCGCGCTCGGTCTAT 16
XX
RESULT 5
ADM94654
ID ADM94654 standard; DNA; 21 BP.
XX
XX ADM94654;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:4.
XX
XX heat shock protein 27; hsp27; cytostatic; gene therapy;
KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
KW antisense oligonucleotide; ss.
XX
XX Homo sapiens.
XX OS Synthetic.
XX
XX WO2004030660-A2.
XX
XX 15-APR-2004.
XX
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PF 02-OCT-2003; 2003WO-CA001588.
XX
XX 02-OCT-2002; 2002US-0415859P.
XX
XX 18-APR-2003; 2003US-0463952P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Gleave ME, Rocchi P, Signaevsky M;
XX WPI; 2004-316331/29.
XX
XX New composition comprising a therapeutic agent that reduces the amount of
PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
PT useful in treating cancer, e.g., prostate cancer or a central nervous
PT system malignancy.
XX
XX Claim 5; SEQ ID NO 4; 38pp; English.
XX
XX The present invention describes a composition which comprises a
CC therapeutic agent that reduces the amount of active heat shock protein 27
CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The
CC composition has cytostatic activity, and can be used in gene therapy. The
CC composition is useful in treating cancer, e.g., prostate, bladder, lung,
CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
CC cancer or a central nervous system malignancy. The present sequence
CC represents a human hsp27 antisense oligonucleotide which is used in the
CC exemplification of the present invention.
XX
XX Sequence 21 BP; 4 A; 5 C; 11 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 75.0%; Score 15; DB 12; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 2.4e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GCGACGCGCGCTCG 15
DB 7 GCGACGCGCGCTCG 21
XX
RESULT 6
ABK52211
ID ABK52211 standard; DNA; 33 BP.
XX
XX ABK52211;
XX
XX 13-AUG-2002 (first entry)
XX
XX Synthetic product 2 reverse PCR primer for construction of pASK-MBD.
XX
XX Mercuric ion; contaminated soil; ground water; hydroponic solution;
KW irrigation water; waste stream; contaminated aqueous medium;
KW biological fluid; gastrointestinal tract; chelon protein;
KW enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
KW heavy metal binding protein; pASK-MBD; PCR; primer; ss.
XX
XX Synthetic.
XX
XX WO200230962-A2.
XX
XX 18-APR-2002.
XX
XX 12-OCT-2001; 2001WO-US031819.
XX
XX 12-OCT-2000; 2000US-0240465P.
XX
XX (UYGE-) UNIV GEORGIA RES FOUND INC.
XX
XX Summers AO, Caguat JJ;
XX WPI; 2002-435437/46.
XX
XX Novel non-naturally occurring recombinant DNA molecule encoding a chelon
PT protein useful for binding divalent cation mercury from contaminated
```

```

PT soil, water, aqueous medium including biological fluids.
XX
XX Disclosure; Page 24; 42pp; English.
XX
CC The present invention relates to a new non-naturally occurring
CC recombinant DNA molecule comprising a sequence encoding a chelon protein
CC which binds mercuric ions. The invention is useful for recombinantly
CC producing a protein in a host-cell, by infecting or transforming a host
CC cell capable of expressing a chelon coding sequence with a vector
CC comprising a promoter active in the host cell operably linked to a coding
CC region for the protein to produce a recombinant host cell and culturing
CC the recombinant host cell under conditions, where DNA is expressed. The
CC nucleic acid encoding the chelon protein is useful for binding divalent
CC mercuric ions, to take up, sequester and concentrate the heavy metal ions
CC from contaminated soil, ground water, hydroponic solutions or irrigation
CC water of waste streams. The DNA of the invention, when immobilised onto a
CC solid support, is useful for concentrating heavy metal ions from
CC contaminated environment waste streams or contaminated aqueous medium
CC including biological fluids. The nucleic acid, when recombinantly
CC expressed in enteric bacteria (which are nontoxicogenic and nonpathogenic),
CC is suitable for use in the in vivo sequestration and elimination of
CC mercuric ion from gastrointestinal tracts of animals or humans exposed to
CC toxic metal ions such as mercury and/or cadmium. The molecules of the
CC invention are also useful in water treatment resins. The nucleic acid of
CC the invention is highly specific and binds divalent cation such as
CC mercury or cadmium with high affinity. The present nucleic acid sequence
CC represents synthetic product 2 reverse PCR primer that was used in the
CC methods of the invention for construction of pASK-MBD vector
XX
XX Sequence 33 BP; 6 A; 8 C; 12 G; 7 T; 0 U; 0 Other;
SQ
Query Match 71.0%; Score 14.2; DB 6; Length 33;
Best Local Similarity 84.2%; Pred. No. 5.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGGACGCGCGGCTCGGTCA 19
Db ||| ||||| ||||| |||||
6 GGGTCTCGCGGCTCGGGCA 24
RESULT 7
ACH58106
ID ACH58106 standard; DNA; 25 BP.
XX
AC ACH58106;
XX
DT 16-OCT-2003 (first entry)
XX
DE DNA target sequence #7242 useful in array for genetic analyses.
XX
KW Gene expression analysis; array; hybridisation; genetic variation;
KW tag-labelled compound; gene family; in situ hybridisation;
KW library screening; Southern hybridisation; northern hybridisation;
KW dot-blot hybridisation; gene sequence; mutation detection;
KW target sequence; probe; PCR; primer; ss.
XX
OS Unidentified.
XX
XX US2003082596-A1.
XX
XX 01-MAY-2003.
XX
XX 08-AUG-2002; 2002US-00215112.
XX
XX 08-AUG-2001; 2001US-0311040P.
XX
XX (MITT/) MITTMANN M.
XX
XX Mittmann M;
XX
XX WPI; 2003-576608/54.
XX
XX New probe array useful e.g. for monitoring gene expression levels, for
PT
PT analyzing genetic variations, or for hybridizing tag-labeled compounds,
PT comprises multiple nucleic acid probes.
XX
XX Claim 1; SEQ ID NO 7242; 9pp; English.
XX
XX The present invention relates to nucleic acid sequences that are
XX complementary to particular genes, and can be used as probes for a
XX variety of analyses such as gene expression analysis. Each probe
XX comprises 9 or more consecutive nucleotides from at least one of 14936
XX nucleotide sequences defined in the patent, or their perfect sense match,
XX sense mismatch, antisense match or antisense mismatch oligonucleotides.
XX The probes may be used in an array comprising at least 10 distinct
XX nucleic acid probes. The array is useful in monitoring gene expression
XX levels by hybridisation to a DNA library, in analysing genetic
XX variations, and in hybridising tag-labelled compounds. The probes are
XX useful for identifying family members of a gene. The probes are also
XX useful in situ hybridisations, in screening cDNA or genomic libraries
XX (or derived subclones) for additional clones containing segments of DNA
XX that have been previously isolated and sequenced, in Southern, northern,
XX or dot-blot hybridisation of genomic DNA to identify or detect the
XX sequence of any gene or detect specific mutations in any gene, and in
XX mapping the 5' termini of mRNA molecules by primer extensions. The
XX nucleic acid sequences of the invention are also useful as PCR primers.
XX The invention provides a large collection of nucleic acid sequences
XX complementary to particular genes with a wide range of analytical uses.
XX ACH50865-ACH65260 represent the target sequences of the invention. Note:
XX The sequence data for this patent was obtained in electronic format
XX directly from the USPTO web site at seqdata.uspto.gov/psipdIDentry.html
XX
XX Sequence 25 BP; 4 A; 9 C; 9 G; 3 T; 0 U; 0 Other;
SQ
Query Match 70.0%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGACGCGCGGCTCG 15
Db ||| ||||| ||||| |||||
2 GGACGCGCGGCTCG 15
RESULT 8
ACI03862/c
ID ACI03862 standard; DNA; 25 BP.
XX
XX ACI03862;
XX
XX 13-OCT-2003 (first entry)
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 3853.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; allelic marker; polymorphism; human;
KW cross-species comparison.
XX
XX Homo sapiens.
XX
XX US2003104410-A1.
XX
XX 05-JUN-2003.
XX
XX 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (AFFY-) AFFYMETRIX INC.
XX
XX Mittmann MP;
XX
XX WPI; 2003-567953/53.
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
XX Southern, Northern or dot-blot hybridization to identify or detect the
XX sequence or specific mutations of any gene.
PT

```


XX Claim 1; SEQ ID NO 3853; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying allelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 6 A; 8 C; 8 G; 3 T; 0 U; 0 Other;
 Query Match 66.0%; Score 13.2; DB 9; Length 25;
 Best Local Similarity 83.3%; Pred. No. 1.6e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 GGACGGCGGCTCGGTCA 19
 |||||
 Db 24 GGACTCGTCTCGGTCA 7
 |||||
 RESULT 9
 ACI65798
 ID ACI65798 standard; DNA; 25 BP.
 XX
 AC ACI65798;
 XX
 DT 14-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 65789.
 XX
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; allelic marker; polymorphism; human;
 KW cross-species comparison.
 XX
 OS Homo sapiens.
 XX
 PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-026759P.
 XX
 PA (APFY-) APFYMATRIX INC.
 XX
 PI Mitmann MP;
 XX
 DR WPI; 2003-567953/53.
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 RS Claim 1; SEQ ID NO 65789; 9pp; English.

XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying allelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 4 A; 8 C; 9 G; 4 T; 0 U; 0 Other;
 Query Match 66.0%; Score 13.2; DB 9; Length 25;
 Best Local Similarity 83.3%; Pred. No. 1.6e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 GACGGCGGCTCGGTCA 20
 |||||
 Db 5 GACCGGAGCTCGGTCT 22
 |||||
 RESULT 10
 AAH21740
 ID AAH21740 standard; DNA; 27 BP.
 XX
 AC AAH21740;
 XX
 DT 14-AUG-2001 (first entry)
 XX
 DE Corynebacterium glutamicum chaperone CpkB related PCR primer SEQ.13.
 XX
 KW Corynebacterium glutamicum; chaperone; chaperonin; CpkB; groEL;
 KW fermentation; L-glutamic acid; thermophilic microbe; PCR primer; ss.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN JP2001069979-A.
 XX
 PD 21-MAR-2001.
 XX
 PF 31-AUG-1999; 99JP-00245121.
 XX
 PR 31-AUG-1999; 99JP-00245121.
 XX
 PA (NISR) JAPAN TOBACCO INC.
 PA (BEAB-) BE ABLE KK.
 XX
 DR WPI; 2001-321175/34.
 XX
 PT Preparation of L-glutamic acid by fermentation.
 XX
 PS Example 1; Page 11; 18pp; Japanese.
 XX
 CC The present invention describes an L-glutamic acid-producing microbe (I)
 CC or its mutant which expresses the molecular chaperone derived from a
 CC thermophilic microbe and produces stably L-glutamic acid at a temperature
 CC near the upper limit of optimum growth or higher. (I) or its mutant
 CC transformed by a recombinant DNA containing a gene encoding the molecular

CC chaperone derived from a thermophilic microbe and a promoter operably
 CC associated with a gene (III) comprising: (a) a fully defined 1661 base
 CC pair (bp) sequence (AAH21757); (b) a nucleic acid sequence encoding a
 CC protein comprising: (i) a base sequence in which 1-20 bases are deleted,
 CC replaced or added in AAH21757; or (ii) at least one base is deleted,
 CC having molecular chaperone activity in (i). Also described is a method
 CC for the preparation of L-glutamic acid by fermentation in which the
 CC transformed (I) is used and cultured at a high temperature limiting the
 CC production of L-glutamic acid with the untransformed (I). The microbe can
 CC be used for the preparation of L-glutamic acid. The present sequence
 CC represents a PCR primer used in the preparation of *Corynebacterium*
 CC glutamicum chaperone CpxB, which is used in an example from the present
 CC invention

XX SQ Sequence 27 BP; 4 A; 9 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 4; Length 27;
 Best Local Similarity 83.3%; Pred. No. 1.6e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GACGGCGCGCTCGTCAT 20
 Db 9 GACGGCGCGACGGCCAT 26
 ||||| |||||

RESULT 11
 AAV51704/c
 ID AAV51704 standard; DNA; 21 BP.

XX AC AAV51704;

XX DT 02-FEB-1999 (first entry)

XX DE Zea mays genome forward PCR primer #304.

XX KW Polymorphic marker; allele-specific; probe; amplification; PCR primer;
 KW hybridisation; plant; hybrid certification; genetic contribution;
 KW progeny; back-cross; hybrid; ancestry; corn; ss.

XX OS Synthetic.

XX OS Zea mays.

XX PN WO9824796-A1.

XX PD 11-JUN-1998.

XX PF 01-DEC-1997; 97WO-US021782.

XX PR 02-DEC-1996; 96US-0032069P.

XX PR 07-MAR-1997; 97US-00813507.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Lemieux B, Landry BS, Sapolsky RJ, Murigneux A;

XX DR WPI; 1998-333252/29.

XX FT Brassica species allele-specific oligonucleotide probes and primers -
 PT useful for plant breeding.

XX PS Example 1; Page 55; 65pp; English.

XX CC AAV51401-V51704 are forward PCR primers used to amplify fragments of the
 CC Zea mays genome in order to detect polymorphic markers. Such markers can
 CC be used in the construction of allele-specific primers and probes for
 CC amplification or hybridisation, e.g. to determine common or disparate
 CC ancestry between 2 or more plants, to monitor the genetic contribution of
 CC an ancestral plant, to trace the progeny of proprietary plants, in
 CC certification of a hybrid plant or to identify the progeny of a back-
 CC crossed plant with an ancestral plant

XX SQ Sequence 21 BP; 3 A; 11 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 2; Length 21;
 Best Local Similarity 87.5%; Pred. No. 2.4e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGG 16
 Db 16 GGGACGCGCGCTCGG 1
 ||||| |||||

RESULT 12
 AAA75395/c
 ID AAA75395 standard; DNA; 23 BP.

XX AC AAA75395;

XX DT 15-JAN-2001 (first entry)

XX DE Fragment derived from the origin of replication of pBR322.

XX KW pBR322 plasmid; probe; primer; origin of replication;

XX KW gene therapy vector; ss.

XX OS Synthetic.

XX PN WO200053803-A1.

XX PD 14-SEP-2000.

XX PF 03-MAR-2000; 2000WO-FR000543.

XX PR 05-MAR-1999; 99FR-00002968.

XX PA (TRGE) TRANSGENE.

XX PI Lamy D;

XX DR WPI; 2000-587445/55.

XX PT Nucleic acid sequences that hybridize to the pBR322 origin of
 PT replication, useful for monitoring gene therapy vectors, and as probes or
 PT primers.

XX PS Claim 3; Page 26; 36pp; French.

XX CC AAA75311-41 and AAA75393-A75402 are derived from the origin of
 CC replication of the pBR322 plasmid. The nucleic acid fragments are useful
 CC as probes and primers for detecting sequences derived from the origin of
 CC replication of pBR322 or vectors (or their fragments) that contain such
 CC sequences. They are particularly used to monitor the presence of gene
 CC therapy vectors (used to deliver therapeutic genes or proteins, antisense
 CC sequences or ribozymes), e.g. for determining disappearance of the
 CC vector, for adjustment of treatment, or for timing of new treatments.
 CC They can also be used to screen foods and cosmetics for the presence of
 CC derived materials from genetically modified organisms

XX SQ Sequence 23 BP; 6 A; 7 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 3; Length 23;
 Best Local Similarity 87.5%; Pred. No. 2.4e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGCGCGCTCGGTCAT 20
 Db 16 CGCTCGCTCGGTCGT 1
 ||||| |||||

RESULT 13
 ABZ58873
 ID ABZ58873 standard; DNA; 24 BP.

XX AC ABZ58873;

DT 27-OCT-2003 (revised)
 XX 28-APR-2003 (first entry)
 DE Zebrafish ZERG mRNA inhibiting antisense oligonucleotide.
 XX
 KW Teleost; zebrafish; ZERG; cardiovascular; antiarrhythmic; cytostatic;
 KW neuroprotective; gene therapy; potassium channel; antisense; ss.
 XX
 OS Danio rerio.
 XX
 XX WO2003006502-A2.
 XX
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2002; 2002WO-IB004280.
 XX
 XX 13-JUL-2001; 2001US-0305396P.
 PR
 XX (ARTE-) ARTEMIS PHARM GMBH.
 PA
 PI Langheinrich U;
 XX
 XX WPI; 2003-210421/20.
 DR
 XX
 XX New teleost (specifically zebrafish) ERG genes, which encode ERG family
 PT potassium channels, useful for studying e.g. cardiac or brain function,
 PT or for developing treatments for e.g. cardiac diseases, cancer or
 PT neurological diseases.
 XX
 PS Claim 7; Page 28; 55pp; English.
 XX
 CC The invention relates to a teleost (zebrafish) ERG (ZERG) polypeptide.
 CC The ZERG nucleic acid molecule is useful for studying cardiac function,
 CC abnormal heart beat phenotype, or long QT syndrome (an abnormality of
 CC cardiac muscle repolarization that predisposes affected individuals to
 CC lethal arrhythmias). The zebrafish comprising ZERG gene is useful as
 CC models for cardiac function or disease. The ZERG genes are particularly
 CC useful for in (non-)cardiac researches, or for developing treatments for
 CC cardiac diseases, tumours or cancers, brain and nervous system disorders
 CC or neurological diseases, or insulin-related diseases. The present
 CC sequence represents the zebrafish ZERG mRNA inhibiting antisense
 CC oligonucleotide. (Updated on 27-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 24 BP; 4 A; 8 C; 9 G; 3 T; 0 U; 0 Other;
 Query Match 64.0%; Score 12.8; DB 8; Length 24;
 Best Local Similarity 87.5%; Pred. No. 2.4e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 CGCGGCGCTCGGTGTCAT 20
 ||||| ||||| |||||
 Db 9 CGCGGCGCACGGGCAT 24
 RESULT 14
 ACI84537/c
 ID ACI84537 standard; DNA; 25 BP.
 AC
 AC ACI84537;
 XX
 DT 14-OCT-2003 (first entry)
 DE
 DE Human microarray DNA oligonucleotide SEQ ID NO 84528.
 XX
 XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX
 OS Homo sapiens.
 XX
 XX US2003104410-A1.
 PN
 XX 05-JUN-2003.

XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFFY-) AFFYMETRIX INC.
 XX
 PI Mittmann MP;
 XX
 XX WPI; 2003-567953/53.
 DR
 XX
 XX New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 XX Claim 1; SEQ ID NO 84528; 9pp; English.
 PS
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 4 A; 9 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 64.0%; Score 12.8; DB 9; Length 25;
 Best Local Similarity 87.5%; Pred. No. 2.4e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GGGACGCGCGCTCGG 16
 ||||| ||||| |||||
 Db 16 GGGACACGGCACTCGG 1
 RESULT 15
 ADO31537
 ID ADO31537 standard; DNA; 29 BP.
 XX
 AC ADO31537;
 XX
 XX 26-AUG-2004 (first entry)
 DT
 DE Human CFTR gene wild-type probe for variant S549N.
 DE
 XX Human; CFTR gene; ss; probe; cystic fibrosis;
 KW Cystic Fibrosis Transmembrane Conductance Regulator;
 KW invasive cleavage structure assay; INVADER; FRET;
 KW fluorescent resonance energy transfer; multiplexed amplification.
 XX
 OS Homo sapiens.
 XX
 XX WO2004046688-A2.
 PN
 XX 03-JUN-2004.
 PD

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OM nucleic - nucleic search, using sw model

Run on: May 8, 2006, 10:10:02 ; Search time 357 Seconds
(without alignments)
228.153 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggacgcgcgcgtcggtcat 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9306428 seqs, 2036268586 residues

Total number of hits satisfying chosen parameters: 13137730

Minimum DB seq length: 0

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA_New.*
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2: /SIDSS/ptodata/2/pubpna/US06_NEW_PUB.seq:2*
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4: /SIDSS/ptodata/2/pubpna/US08_NEW_PUB.seq:4*
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6: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq:6*
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19: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq:19*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	18	US-11-262-388-82
2	20	100.0	21	18	US-11-262-388-81
3	19	95.0	19	18	US-11-262-388-90
4	16	80.0	21	18	US-11-262-388-3
5	15.2	76.0	22	10	US-10-310-914A-649206
6	15.2	76.0	25	17	US-11-121-849-405955
7	15	75.0	21	18	US-11-262-388-4
8	14.8	74.0	23	10	US-10-310-914A-1230089
9	14.4	72.0	18	10	US-10-310-914A-940948
10	14.4	72.0	21	10	US-10-310-914A-1294776
11	14.4	72.0	22	10	US-10-310-914A-597930
12	14.4	72.0	24	10	US-10-310-914A-940913
13	14	70.0	22	10	US-10-310-914A-185611
14	13.8	69.0	24	10	US-10-310-914A-279177

15	13.8	69.0	24	10	US-10-310-914A-279178	Sequence 279178,
16	13.8	69.0	24	10	US-10-310-914A-279179	Sequence 279179,
17	13.8	69.0	24	10	US-10-310-914A-279180	Sequence 279180,
18	13.8	69.0	25	11	US-10-932-182A-16224	Sequence 16224, A
19	13.8	69.0	25	11	US-10-932-182A-16224	Sequence 16224, A
20	13.8	69.0	25	17	US-11-121-849-405692	Sequence 405692,
21	13.6	68.0	21	10	US-10-310-914A-371039	Sequence 371039,
22	13.6	68.0	21	10	US-10-310-914A-1263762	Sequence 1263762,
23	13.4	67.0	19	10	US-10-310-914A-625756	Sequence 625756,
24	13.4	67.0	20	10	US-10-310-914A-968771	Sequence 968771,
25	13.4	67.0	22	18	US-11-148-423-82	Sequence 82, Appl
26	13.4	67.0	26	10	US-10-310-914A-1239636	Sequence 1239636,
27	13.4	67.0	30	14	US-11-226-605-70	Sequence 70, Appl
28	13.2	66.0	18	10	US-10-310-914A-1303083	Sequence 1303083,
29	13.2	66.0	19	10	US-10-310-914A-41833	Sequence 41833, A
30	13.2	66.0	21	10	US-10-310-914A-615113	Sequence 615113,
31	13.2	66.0	24	10	US-10-310-914A-62912	Sequence 62912, A
32	13.2	66.0	25	10	US-10-310-914A-839926	Sequence 839926,
33	13.2	66.0	25	17	US-11-121-849-39050	Sequence 39050, A
34	13.2	66.0	25	17	US-11-121-849-143212	Sequence 143212,
35	13.2	66.0	25	17	US-11-136-527-297166	Sequence 297166,
36	13	65.0	25	11	US-10-933-982-120239	Sequence 120239,
37	13	65.0	25	11	US-10-933-982-151912	Sequence 151912,
38	13	65.0	25	11	US-10-933-982-201040	Sequence 201040,
39	13	65.0	25	11	US-10-934-048A-115670	Sequence 115670,
40	12.8	64.0	18	10	US-10-310-914A-60726	Sequence 60726, A
41	12.8	64.0	18	10	US-10-310-914A-721661	Sequence 721661,
42	12.8	64.0	19	10	US-10-310-914A-60727	Sequence 60727, A
43	12.8	64.0	19	10	US-10-310-914A-60744	Sequence 60744, A
44	12.8	64.0	19	10	US-10-310-914A-261943	Sequence 261943,
45	12.8	64.0	19	10	US-10-310-914A-984231	Sequence 984231,

ALIGNMENTS

RESULT 1

US-11-262-388-82
; Sequence 82, Application US/11262388
; Publication No. US2006004086A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; TITLE OF INVENTION: Cancers
; FILE REFERENCE: UBC.P-031
; CURRENT APPLICATION NUMBER: US/11/262,388
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: US/10/605,498
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-262-388-82

Query Match 100.0%; Score 20; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCAAT 20

Db 1 GGGACGCGCGCTCGGTCAAT 20

RESULT 2

```
US-11-262-388-81
; Sequence 81, Application US/11262388
; Publication No. US20060040886A1
; GENERAL INFORMATION:
; APPLICANT: Gleeve, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; TITLE OF INVENTION: Cancers
; FILE REFERENCE: UBC.P-031
; CURRENT APPLICATION NUMBER: US/11/262,388
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: US/10/605,498
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-262-388-81

Query Match      100.0%; Score 20; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCAAT 20
   |||||
Db 2 GGGACGGCGGCTCGGTCAAT 21

RESULT 3
US-11-262-388-90/c
; Sequence 90, Application US/11262388
; Publication No. US20060040886A1
; GENERAL INFORMATION:
; APPLICANT: Gleeve, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; TITLE OF INVENTION: Cancers
; FILE REFERENCE: UBC.P-031
; CURRENT APPLICATION NUMBER: US/11/262,388
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: US/10/605,498
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-262-388-90

Query Match      95.0%; Score 19; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACGGCGGCTCGGTCAAT 20
   |||||
Db 19 GGACGGCGGCTCGGTCAAT 1

RESULT 4
US-11-262-388-81
```

```
; Sequence 3, Application US/11262388
; Publication No. US20060040886A1
; GENERAL INFORMATION:
; APPLICANT: Gleeve, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; TITLE OF INVENTION: Cancers
; FILE REFERENCE: UBC.P-031
; CURRENT APPLICATION NUMBER: US/11/262,388
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: US/10/605,498
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-262-388-3

Query Match      80.0%; Score 16; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGCGGCGGCTCGGTCAAT 20
   |||||
Db 1 CGCGGCGGCTCGGTCAAT 16

RESULT 5
US-10-310-914A-649206/c
; Sequence 649206, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvyzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 649206
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-649206

Query Match      76.0%; Score 15.2; DB 10; Length 22;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCAAT 20
   |||||
Db 21 GGGACGGCGGCTCGGCCAT 2

RESULT 6
US-11-121-849-405955/c
; Sequence 405955, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
```



```
;; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 597930
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-597930

Query Match          72.0%; Score 14.4; DB 10; Length 22;
Best Local Similarity 93.8%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGG 16
   |||||
Db 22 GGGACGCGCGCTCGG 7

RESULT 12
US-10-310-914A-940913/c
; Sequence 940913, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 940913
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-940913

Query Match          72.0%; Score 14.4; DB 10; Length 24;
Best Local Similarity 93.8%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGG 16
   |||||
Db 19 GGGACGCGCGCTGG 4

RESULT 13
US-10-310-914A-185611
; Sequence 185611, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 185611
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
```

```
US-10-310-914A-185611

Query Match          70.0%; Score 14; DB 10; Length 22;
Best Local Similarity 92.9%; Pred. No. 2e+03;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTC 14
   |||||
Db 8 GGGACGCGCGCUC 21

RESULT 14
US-10-310-914A-279177
; Sequence 279177, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 279177
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-279177

Query Match          69.0%; Score 13.8; DB 10; Length 24;
Best Local Similarity 82.4%; Pred. No. 2.5e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGACGCGCGCTCGGTC 18
   |||||
Db 6 GGACGCGCGCGGUC 22

RESULT 15
US-10-310-914A-279178
; Sequence 279178, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 279178
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-279178

Query Match          69.0%; Score 13.8; DB 10; Length 24;
Best Local Similarity 82.4%; Pred. No. 2.5e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGACGCGCGCTCGGTC 18
   |||||
Db 6 GGACGCGCGCGGUC 22

Search completed: May 8, 2006, 10:20:49
Job time : 357 secs
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2006, 09:37:03 ; Search time 1958 Seconds
(without alignments)
477.907 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggacgagcgctcggtcat 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 78772

Minimum DB seq length: 0

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	12.8	64.0	32	2	BF131807
C 2	12.4	62.0	26	10	AG203073
C 3	12.2	61.0	28	1	AI287864
C 4	12.0	60.0	31	1	AA867755
C 5	11.4	57.0	31	10	CZ169504
C 6	11.4	57.0	31	9	AZ826864
C 7	11.2	56.0	23	10	AJ587908
C 8	11.2	56.0	31	6	CD028820
C 9	11.1	55.0	21	9	AZ420773
C 10	11.1	55.0	33	10	AJ599957
C 11	11.1	55.0	34	1	AA259780
C 12	10.6	53.0	25	1	AI758887
C 13	10.6	53.0	25	6	CF643223
C 14	10.6	53.0	29	6	CF643257
C 15	10.6	53.0	33	10	AG216212
C 16	10.6	53.0	35	6	CF298077
C 17	10.6	53.0	35	6	CF642505
C 18	10.6	53.0	35	8	DR108402
C 19	10.4	52.0	22	3	BM398778
C 20	10.4	52.0	26	10	CG731752
C 21	10.4	52.0	27	11	TA103C01P
C 22	10.4	52.0	28	1	AI256473

23	10.4	52.0	29	9	CC456807	CC456807 SALK_1007
C 24	10.4	52.0	31	10	CG724391	CG724391 1115081A0
C 25	10.4	52.0	34	8	N55046	N55046 yz20g11.x1
C 26	10.4	52.0	34	9	AZ346691	AZ346691 1M0082103
C 27	10.2	51.0	25	1	AI002379	AI002379 Q87F02.8
C 28	10.2	51.0	27	6	CF277108	CF277108 14ETL--02
C 29	10.2	51.0	28	1	AB080287	AB080287 AB080287
C 30	10.2	51.0	28	1	AI358659	AI358659 QX6007.X
C 31	10.2	51.0	29	1	AW246529	AW246529 2821891.3
C 32	10.2	51.0	30	1	AJ746806	AJ746806 AJ746806
C 33	10.2	51.0	30	10	CZ472135	CZ472135 G01278-5p
C 34	10.2	51.0	31	1	AA912813	AA912813 0143502.8
C 35	10.2	51.0	31	3	BI915569	BI915569 603176924
C 36	10.2	51.0	33	10	AJ600534	AJ600534 Arabidops
C 37	10.2	51.0	33	11	DME545177	DME545177 Arabidops
C 38	10.2	51.0	34	1	AA737625	AA737625 085201.8
C 39	10.2	51.0	34	10	CG712020	CG712020 111902360
C 40	10.0	50.0	21	9	AZ513847	AZ513847 1M0360D08
C 41	10.0	50.0	22	8	DR103042	DR103042 JHU009E01
C 42	10.0	50.0	27	9	AZ769255	AZ769255 1M0569B17
C 43	10.0	50.0	30	1	AJ746842	AJ746842 AJ746842
C 44	10.0	50.0	30	10	CZ472687	CZ472687 d02227-3p
C 45	10.0	50.0	30	10	CZ488898	CZ488898 f06234-5p

ALIGNMENTS

RESULT 1
BF131807/c

LOCUS

DEFINITION

601820724F1 NIH_MGC_58 Homo sapiens

mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF131807 32 bp mRNA linear EST 24-OCT-2000
601820724F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052596 5',
mRNA sequence.

BF131807
BF131807.1 GI:10970847
EST.
Homo sapiens (human)

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

1 (bases 1 to 32)
NIH-MGC http://mgc.mci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: L1CM889 row: p column: 05
High quality sequence start: 8
High quality sequence stop: 30.

Location/Qualifiers
1..32
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4052596"
/tissue_type="hypertrophied"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_58"

/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctggcc); Site_2: SfiI (ggccattggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTAGAGCGGCGGCACATG-DT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average

insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 64.0%; Score 12.8; DB 2; Length 32;
Best Local Similarity 87.5%; Pred. No. 2.5e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGCGGCGCTCGGTTCAT 20
|||||
Db 27 CGCTCGGCTCGGTCT 12

RESULT 2

AG203073

LOCUS

DEFINITION Pan troglodytes DNA, clone: RP43-087B01.T7, genomic survey
sequence.

ACCESSION

AG203073

VERSION

AG203073.1 GI:45235248

KEYWORDS

GSS.

SOURCE

Pan troglodytes (chimpanzee)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.

REFERENCE

1

AUTHORS

Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C. J.,
Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

TITLE

BAC end sequences of Library RP-43

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 26)

AUTHORS

Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C. J.,
Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

TITLE

Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail: redstone@mail.krribb.re.kr, URL: http://phs.grc.krribb.re.kr/,
Tel: 82-42-866-7181, Fax: 82-42-860-4409)

JOURNAL

Clones are derived from the chimpanzee BAC library RP-43. This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.

COMMENT

PRIMERS

LIBRARY

Sequencing: T7

Vector

: pBACe3.6

R.Site 1

: EcoRI

R.Site 2

: EcoRI

Location/Qualifiers

1..26

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

/clone="RP43-087B01.T7"

/sex="male"

/cell_type="lymphocytes"

/clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 62.0%; Score 12.4; DB 10; Length 26;

Best Local Similarity 92.9%; Pred. No. 3.9e+05;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGACGCGCGCTC 14

|||||

Db 1 GCGACTCGCGCTC 14

|||||

RESULT 3

AI287864/c

LOCUS

DEFINITION

qv07dl2.x1 NCI CGAP Kid8 Homo sapiens cDNA clone IMAGE:190887 3',
similar to SW:CA44 HUMAN P53420 COLLAGEN ALPHA 4 (IV) CHAIN
PRECURSOR. ; contains MER22.b3 TAR1 repetitive element ; mRNA
sequence.

ACCESSION

AI287864

VERSION

AI287864.1 GI:3927617

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1 (bases 1 to 28)

AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

FEATURES

source

1..28

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:190887"

/tissue_type="renal cell tumor"

/lab_host="DH10B"

/clone_lib="NCI CGAP Kid8"

/note="Organ: Kidney; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.2 Kb. Life technologies catalog #:
11524-014"

ORIGIN

Query Match 61.0%; Score 12.2; DB 1; Length 28;

Best Local Similarity 82.4%; Pred. No. 4.7e+05;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGT 17

|||||

Db 21 GGGCGGGGGCGCGGT 5

|||||

RESULT 4

AA867755/c

LOCUS

AA867755

DEFINITION

vx16b08.r1 Soares thymus 2NbMT Mus musculus cDNA clone
IMAGE:1264599 5' similar to TR:O35394 O35394 PRENYLATED RAB
ACCEPTOR 1. ; mRNA sequence.

ACCESSION

AA867755

VERSION

AA867755.1 GI:2963200

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 31)

AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

AI287864 28 bp mRNA linear EST 24-NOV-1998
qv07dl2.x1 NCI CGAP Kid8 Homo sapiens cDNA clone IMAGE:190887 3',
similar to SW:CA44 HUMAN P53420 COLLAGEN ALPHA 4 (IV) CHAIN
PRECURSOR. ; contains MER22.b3 TAR1 repetitive element ; mRNA
sequence.

AI287864

AI287864.1 GI:3927617

EST.

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 28)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers

1..28

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:190887"

/tissue_type="renal cell tumor"

/lab_host="DH10B"

/clone_lib="NCI CGAP Kid8"

/note="Organ: Kidney; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.2 Kb. Life technologies catalog #:
11524-014"

Query Match 61.0%; Score 12.2; DB 1; Length 28;

Best Local Similarity 82.4%; Pred. No. 4.7e+05;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGT 17

|||||

Db 21 GGGCGGGGGCGCGGT 5

|||||

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LMANL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:667151

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

FEATURES

```

1. .31
  /organism="Mus musculus"
  /mol_type="mRNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="IMAGE:1264599"
  /sex="male"
  /tissue_type="Thymus"
  /dev_stage="4 weeks"
  /lab_host="DH10B"
  /notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAATGGAGCGCGCGTGTGTGTGTGTGTGTGTGTGTGTGT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."
```

ORIGIN

```

Query Match          60.0%; Score 12; DB 1; Length 31;
Best Local Similarity 75.0%; Pred. No. 5.7e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```

QY 1 GGGACGGCGCGCTCGGTCTAT 20
    ||||| ||||| ||||| |||||
Db 20 GGGTCGTGGCGCTCAGCCCT 1
```

```

RESULT 5
CZ169504/c
LOCUS          31 bp mRNA linear GSS 22-MAR-2005
DEFINITION    G050C04 GGTC Gene Trap Library GV07C05 Mus musculus cDNA clone
G050C04, mRNA sequence.
ACCESSION     CZ169504
VERSION       CZ169504.2 GI:61685966
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
```

```

REFERENCE
AUTHORS        Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,
Arnold, H.H., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.
A large-scale, gene-driven mutagenesis approach for the functional
analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
12904583
COMMENT        On Mar 22, 2005 this sequence version replaced gi:58224102.
```

Contact: GGTC

German Genetrap Consortium (GGTC)

Email: info@genetrap.de

U3CEO gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at:

'http://genetrap.gsf.de/project/web_new/database/result_clone.html?clone_id=G050C04' ES cell line harboring insertion mutation of target gene is available at:

'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm'

1' Inhouse Sequence Identifier: 16629

Class: Gene trap.

Location/Qualifiers

```

1. .31
  /organism="Mus musculus"
  /mol_type="mRNA"
  /strain="129 Sv"
  /db_xref="taxon:10090"
  /clone="G050C04"
  /sex="Male"
  /cell_type="Embryonic stem cell"
  /cell_line="ES cells [C57BL/6J x 129Sv/SvEvTac] F1"
  /clone_lib="GGTC Gene Trap Library GV07C05"
  /note="Vector: U3CEO"
```

ORIGIN

```

Query Match          60.0%; Score 12; DB 10; Length 31;
Best Local Similarity 75.0%; Pred. No. 5.7e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```

QY 1 GGGACGGCGCGCTCGGTCTAT 20
    ||||| ||||| ||||| |||||
Db 29 GGGACGGCGCGGTTCACAT 10
```

RESULT 6

```

AZ826864
2M0102H20R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0102H20 R, genomic survey sequence.
DEFINITION
ACCESSION     AZ826864
VERSION       AZ826864.1 GI:12996772
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
```

REFERENCE

```

AUTHORS        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0102 row: H column: 20
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.
Location/Qualifiers
```

FEATURES

```

1. .31
  /organism="Mus musculus"
  /mol_type="genomic DNA"
  /strain="C57BL/6J"
```

```

/db_xref="taxon:10090"
/clone="UUGC2M0102H20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 57.0%; Score 11.4; DB 9; Length 31;
Best Local Similarity 92.3%; Pred. No. 1.1e+06;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCT 13
|||||
Db 19 GGGACGCGTGCT 31

RESULT 7
AJ587908/c
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 339810, genomic survey sequence.
ACCESSION
AJ587908
VERSION
AJ587908.1 GI:37937532
KEYWORDS
GSS: left border; T-DNA flanking sequence.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eutrosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1
AUTHORS
Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL
EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED
12446565
REFERENCE
2 (bases 1 to 23)
AUTHORS
Balzerque,S.
TITLE
Direct Submission
JOURNAL
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
source

1..23
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="339810"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
1..23
/notes="T-DNA flanking sequence
left border"

misc_feature
56.0%; Score 11.2; DB 10; Length 23;
Best Local Similarity 81.2%; Pred. No. 1.4e+06;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ORIGIN
Query Match
Best Local Similarity
Matches
QY 1 GGGACGCGCGCTCGG 16
|||||
Db 21 GGGACGCGCGCATGG 6

RESULT 8
CD028820
LOCUS
DEFINITION
mgmy006xA17f.b Magnaporthe grisea MY Uni-Zap XR Library Magnaporthe grisea CDNA clone mgmy006xA17 5', mRNA sequence.
ACCESSION
CD028820
VERSION
CD028820.1 GI:30410276
KEYWORDS
EST.
SOURCE
Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE
1 (bases 1 to 31)
AUTHORS
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
TITLE
Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
JOURNAL
Unpublished (2002)
COMMENT
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person;
PCR Primers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgmy006 row: A column: 17
Seq primer: T3.
Location/Qualifiers
source

1..31
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strains="70-15"
/db_xref="taxon:148305"
/clone="mgmy006xA17"
/sex="Mat1-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnaporthe grisea MY Uni-Zap XR Library"
/notes="Vector: pBluescriptSK+; Site_1: EcoRI; Site_2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Minimal medium mycelium library. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

```

ORIGIN

Query Match 56.0%; Score 11.2; DB 6; Length 31;
 Best Local Similarity 81.2%; Pred. No. 1.3e+06;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CGCGGGCTCGGTTCAT 20
 | | | | | | | | | |
 Db 6 CTCGGCGTTGGTTCAT 21

RESULT 9
AZA20773/c

LOCUS
 DEFINITION 21 bp DNA linear GSS 03-OCT-2000
 1M0198E18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0198E18 R, genomic survey sequence.

ACCESSION AZA20773
 VERSION AZA20773.1 GI:10544786

KEYWORDS
 SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1 Dunin, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0198 row: E column: 18

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

source

1..21
 Location/Qualifiers

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0198E18"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells

ORIGIN

Query Match 55.0%; Score 11; DB 9; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGCGCGC 11
 | | | | | | | | | |
 Db 16 GGGACGCGCGC 6

and selected for ampicillin resistance."

RESULT 10

AJ599957

LOCUS

DEFINITION 33 bp DNA linear GSS 15-JAN-2004

Arabidopsis thaliana T-DNA flanking sequence, left border, clone

497C08, genomic survey sequence.

ACCESSION AJ599957

VERSION AJ599957.1 GI:37949585

KEYWORDS GSS; left border; T-DNA flanking sequence.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE

AUTHORS

1 Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
 Chauvin, S., Reichtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
 Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis A.

of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)

12446565

2 (bases 1 to 33)

Balzergue, S.

Direct Submission

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
 Gaston Cremieux, 91057 Evry cedex, FRANCE
 PCR was performed on DNA from transformants of Arabidopsis thaliana
 plants from INRA (Versailles). The DNA fragment(s) resulting from
 the PCR were directly sequenced from the left or the right border
 to determine the genomic sequence flanking the insertion. T-DNA
 derived sequences were removed. Information to order the
 corresponding mutant line and a link to a database providing a
 graphical display of the insertion site are available at
 http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
 been generated in the framework of the French plant genomics
 program 'Genoplante' (http://www.genoplante.com and
 http://genoplante-info.infobiogen.fr).

FEATURES

source

1..33
 Location/Qualifiers

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

/clone="497C08"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Massilewskija"

1..33

misc_feature

/note="T-DNA flanking sequence

left border"

ORIGIN

Query Match 55.0%; Score 11; DB 10; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGCGCGC 11

| | | | | | | | | |

Db 23 GGGACGCGCGC 33

RESULT 11

AA259780/c

```

LOCUS      AA259780              34 bp      mRNA      linear      EST 18-MAR-1997
DEFINITION      Ya87b10.r1 Soares mouse 3NBE12.5 Mus musculus cDNA clone
                  IMAGE:746395 5' similar to TR:G971986 G971986 NADH DEHYDROGENASE ;,
                  mRNA sequence.
ACCESSION      AA259780
VERSION        AA259780.1 GI:1896266
KEYWORDS       EST.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 34)
AUTHORS        Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
               Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
               Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
               Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
               Waterston,R.
TITLE          The WashU-HHMI Mouse EST Project
JOURNAL        Unpublished (1996)
COMMENT        Contact: Marra M/Mouse EST Project
               WashU-HHMI Mouse EST Project
               Washington University School of Medicine
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
               Tel: 314 286 1800
               Fax: 314 286 1810
               Email: mouseest@watson.wustl.edu
               This clone is available royalty-free through LNL; contact the
               IMAGE Consortium (info@image.llnl.gov) for further information.
               MGI:455379
FEATURES       Trace considered overall poor quality
               Possible reversed clone: similarity on wrong strand
               Seq primer: -28ml3 rev2 ET from Amersham
               High quality sequence stop: 1.
               Location/Qualifiers
               1..34
               /organism="Mus musculus"
               /mol_type="mRNA"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="IMAGE:746395"
               /sex="unknown"
               /tissue_type="fetus"
               /dev_stage="12.5dpc total fetus"
               /lab_host="DH10B"
               /clone_lib="Soares mouse 3NBE12 5"
               /note="Organ: whole fetus; Vector: pT7T3D-Pac (Pharmacia)
               with a modified polylinker; Site 1: Not I; Site 2: Eco RI;
               1st strand cDNA was primed with a Not I - oligo(dT) primer
               [5' TGTTACCAATCTGAGTGGAGCGCGCCCTATTATTTTATTTTATTTT
               3'], on total mouse RNA [provided by Minoru Ko, Wayne
               State Univ.]; double-stranded cDNA was ligated to Eco RI
               adaptors (Pharmacia), digested with Not I and cloned into
               the Not I and Eco RI sites of the modified pT7T3 vector.
               Library went through one round of normalization, and was
               constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN
Query Match      55.0%; Score 11; DB 1; Length 34;
Best Local Similarity 73.7%; Pred. No. 1.6e+06;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 GGGACGGCGGCTCGTCA 19
        ||||| ||| |||||
DB      34 GGGACTCAGCTCATGTCA 16

RESULT 12
AI758887      25 bp      mRNA      linear      EST 23-JUN-1999
LOCUS         ty94c11.x1 NCI CGAP Utl Homo sapiens cDNA clone IMAGE:2286740 3',
DEFINITION     similar to TR:Q64371 Q64371 PR-VBETAL. ;contains element TAR1
               repetitive element ;, mRNA sequence.
ACCESSION      AI758887
VERSION        AI758887.1 GI:5152612
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominoidea; Homo.
REFERENCE      1 (bases 1 to 25)
AUTHORS        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
               National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
               Unpublished (1997)
JOURNAL        Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-remail.nih.gov
               Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
               Emmert-Buck, M.D., Ph.D.
               cDNA Library Preparation: Life Technologies, Inc.
               DNA Sequencing by: Greg Lennon, Ph.D.
               DNA Sequencing by: Washington University Genome Sequencing Center
               Clone distribution: NCI-CGAP clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               www-bio.llnl.gov/bbrp/image/image.html
               Trace considered overall poor quality
               Seq primer: -40UP from Gibco
               High quality sequence stop: 1.
               Location/Qualifiers
               1..25
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:2286740"
               /tissue_type="well-differentiated endometrial
               adenocarcinoma, 7 pooled tumors"
               /lab_host="DH10B"
               /clone_lib="NCI CGAP Utl"
               /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
               Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
               Average insert size 1.75 kb. Life Technologies catalog #:
               11538-014"
ORIGIN
Query Match      53.0%; Score 10.6; DB 1; Length 25;
Best Local Similarity 76.5%; Pred. No. 2.5e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GGGACGGCGGCTCGGT 17
        ||| ||||| |||||
DB      5 GGGGGGGCGCGCGCGGT 21

RESULT 13
CF643223/c
LOCUS          CF643223 25 bp      mRNA      linear      EST 02-OCT-2003
DEFINITION     D61_D08 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
               sequence.
ACCESSION      CF643223
VERSION        CF643223.1 GI:37411328
KEYWORDS       EST.
SOURCE         Ustilago maydis
ORGANISM       Ustilago maydis
               Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
               Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
REFERENCE      1 (bases 1 to 25)
AUTHORS        Nugent,K.G., Choffe,K. and Saville,B.J.
TITLE          Gene expression during Ustilago maydis diploid filamentous growth:
               EST library creation and analyses
JOURNAL        Fungal Genet. Biol. 41 (3), 349-360 (2004)
COMMENT        14761795
               Contact: Barry J. Saville
               Saville Lab
               University of Toronto

```

3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
 Tel: 905 569 4702
 Fax: 905 828 3792
 Email: bsaville@utm.utoronto.ca
 Plate: UTM-UM-D126/7-061-UTM row: 08 column: D
 Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGG 3')
 High quality sequence stop: 25.
 Location/Qualifiers

FEATURES

source

1. .25

/organism="Ustilago maydis"
 /mol_type="mRNA"
 /strain="FBD12"
 /db_xref="taxon:5270"
 /cell_type="Mycelia"
 /dev_stage="Filamentous diploid"
 /clone_lib="Filamentous Forced Diploid"
 /notes="Vector: pSport; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

ORIGIN

Query Match 53.0%; Score 10.6; DB 6; Length 25;
 Best Local Similarity 76.5%; Pred. No. 2.5e+06;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 GGACGGCGGCTCGGTC 18
 ||||| |
 Db 24 GGACGGCTGGTCGATC 8

RESULT 14

CF643257/c

LOCUS

DEFINITION

D62_B05 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

COMMENT

29 bp mRNA linear EST 02-OCT-2003
 Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 Nugent.K.G., Choffe,K. and Saville,B.J.
 Gene expression during Ustilago maydis diploid filamentous growth:
 EST library creation and analyses
 Fungal Genet. Biol. 41 (3), 349-360 (2004)
 14761795
 Contact: Barry J. Saville
 Saville Lab
 University of Toronto
 3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
 Tel: 905 569 4702
 Fax: 905 828 3792
 Email: bsaville@utm.utoronto.ca
 Plate: UTM-UM-D126/7-062-UTM row: 05 column: B
 Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGG 3')
 High quality sequence stop: 29.
 Location/Qualifiers

FEATURES

source

1. .29

/organism="Ustilago maydis"
 /mol_type="mRNA"
 /strain="FBD12"
 /db_xref="taxon:5270"
 /cell_type="Mycelia"
 /dev_stage="Filamentous diploid"
 /clone_lib="Filamentous Forced Diploid"
 /notes="Vector: pSport; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

ORIGIN

Query Match 53.0%; Score 10.6; DB 6; Length 29;
 Best Local Similarity 76.5%; Pred. No. 2.5e+06;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 GGACGGCGGCTCGGTC 18
 ||||| |
 Db 28 GGACGGCTGGTCGATC 12

FEATURES

source

15

AG216212/c

LOCUS

DEFINITION

Drosophila melanogaster DNA, clone:NP1197-5-1, flanking P[GaWB]

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

COMMENT

FEATURES

source

1. .33

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/strain="NP1197"

/db_xref="taxon:7227"

/chromosome="2"

/map="54C6"

/clone="NP1197-5-1"

/note="flanking P[GaWB] transposon insertion"

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY

2

GGACGGCGGCTCGGTC

18

Db

22

GCATCGTCGACGGTC

6

Search completed: May

Job time : 1959 secs

8, 2006, 10:09:50

HIS PAGE BLANK (USPTO)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2006, 09:47:57 ; Search time 96 Seconds
(without alignments)
370.325 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggacgcgctcggtcat 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1097522

Minimum DB seq length: 0

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	14	70.0	25	3	US-09-396-196G-42173
C 3	13.8	69.0	25	3	US-09-396-196G-46323
C 4	13.8	69.0	25	3	US-09-396-196G-46324
C 5	13.8	69.0	25	3	US-09-396-196G-46335
C 6	13.2	66.0	25	3	US-09-396-196G-53301
7	13	65.0	20	3	US-09-046-858A-19
8	13	65.0	20	3	US-09-450-515-19
9	13	65.0	20	3	US-10-206-654-19
10	12.6	63.0	20	3	US-10-131-827-8773
C 11	12.6	63.0	24	3	US-09-540-014-35
C 12	12.6	63.0	24	3	US-09-164-210-12
C 13	12.6	63.0	24	3	US-09-538-864-14
C 14	12.6	63.0	24	3	US-10-091-841A-35
C 15	12.6	63.0	25	3	US-09-396-196G-40648
C 16	12.6	63.0	30	3	US-09-319-648-52
17	12.6	63.0	30	9	5240848-8
18	12.4	62.0	20	2	US-08-182-175A-9
19	12.4	62.0	20	2	US-08-474-633A-16
20	12.4	62.0	20	3	US-08-823-771-16
21	12.4	62.0	20	6	PCT-US92-06412-9
C 22	12.4	62.0	25	3	US-09-396-196G-41065
C 23	12.4	62.0	25	3	US-09-396-196G-46162
C 24	12.4	62.0	25	3	US-09-396-196G-46163

25	12.2	61.0	21	3	US-09-158-863C-38	Sequence 38, Appl
C 26	12.2	61.0	22	3	US-09-589-560B-58	Sequence 58, Appl
C 27	12.2	61.0	22	3	US-09-589-560B-62	Sequence 62, Appl
C 28	12.2	61.0	25	3	US-09-396-196G-25195	Sequence 25195, A
C 29	12.2	61.0	25	3	US-09-396-196G-49392	Sequence 49392, A
C 30	12.2	61.0	34	3	US-09-487-558B-3	Sequence 3, Appli
C 31	12	60.0	23	3	US-09-462-671-1	Sequence 1, Appli
C 32	12	60.0	27	3	US-08-485-355B-4	Sequence 4, Appli
C 33	12	60.0	29	3	US-09-045-583-45	Sequence 45, Appl
34	12	60.0	29	3	US-09-534-185-45	Sequence 45, Appl
C 35	12	60.0	32	3	US-08-485-355B-30	Sequence 30, Appl
C 36	12	60.0	32	3	US-09-045-583-44	Sequence 44, Appl
C 37	12	60.0	32	3	US-09-534-185-44	Sequence 44, Appl
C 38	11.8	59.0	17	2	US-08-171-299B-6	Sequence 6, Appli
C 39	11.8	59.0	20	3	US-09-467-642-13	Sequence 13, Appl
C 40	11.8	59.0	23	3	US-08-930-797B-2	Sequence 2, Appli
C 41	11.8	59.0	27	2	US-08-580-401-5	Sequence 5, Appli
C 42	11.8	59.0	27	2	US-08-927-394-8	Sequence 8, Appli
C 43	11.8	59.0	31	2	US-08-927-394-7	Sequence 7, Appli
C 44	11.6	58.0	18	3	US-09-402-618B-75	Sequence 75, Appl
C 45	11.6	58.0	18	3	US-09-942-588A-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1

US-09-977-137A-16
; Sequence 16, Application US/09977137A
; Patent No. 6750042
; GENERAL INFORMATION:
; APPLICANT: Summers, Anne O.
; APPLICANT: Caguiat, Jonathan
; TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 79-00
; CURRENT APPLICATION NUMBER: US/09/977,137A
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,465
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-977-137A-16

Query Match 71.0%; Score 14.2; DB 3; Length 33;
Best Local Similarity 84.2%; Pred. No. 3e+03; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3

QY 1 GGGACGCGCGCTCGGTCA 19
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Db 6 GGGTCTCGCGCTCGGGCA 24

RESULT 2

US-09-396-196G-42173/c
; Sequence 42173, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678

Query Match 70.0%; Score 14; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CGCGCGCTCGGTTCAT 20
DB 20 CGCGCGCTCGGTTCAT 7

RESULT 3
US-09-396-196G-46323/c
; Sequence 46323, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46323
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-46323

Query Match 69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGCGCGCTCGGTTCAT 20
DB 20 ACGCTGCGCACGGTTCAT 4

RESULT 4
US-09-396-196G-46324/c
; Sequence 46324, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46324
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-46324

Query Match 69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGCGCGCTCGGTTCAT 20
DB 18 ACGCTGCGCACGGTTCAT 2

Query Match 69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGCGCGCTCGGTTCAT 20
DB 19 ACGCTGCGCACGGTTCAT 3

RESULT 5
US-09-396-196G-46335/c
; Sequence 46335, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46335
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-46335

Query Match 69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGCGCGCTCGGTTCAT 20
DB 18 ACGCTGCGCACGGTTCAT 2

RESULT 6
US-09-396-196G-53301
; Sequence 53301, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53301
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-53301

Query Match 66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 8.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GACCGCGCGCTCGGTTCAT 20
DB 2 GACCCAGCGCTCTGTTCAT 19

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RESULT 7
US-09-046-858A-19
; Sequence 19, Application US/09046858A
; Patent No. 6048973
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
; IN ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: PO Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,858A
; FILING DATE: 24-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/042,376
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 2000-0456.30
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-046-858A-19
Query Match 65.0%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACGCGGCGCTCG 15
Db 2 GACGCGGCGCTCG 14

RESULT 8
US-09-450-515-19
; Sequence 19, Application US/09450515
; Patent No. 6680425
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
; IN ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: PO Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/206,654
; FILING DATE: 25-JUL-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,858A
; FILING DATE: 24-MAR-1998
; APPLICATION NUMBER: 60/042,376
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 2000-0456.30
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-450-515-19
Query Match 65.0%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACGCGGCGCTCG 15
Db 2 GACGCGGCGCTCG 14

RESULT 9
US-10-206-654-19
; Sequence 19, Application US/10206654
; Patent No. 6919493
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
; IN ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: PO Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/206,654
; FILING DATE: 25-JUL-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,858A
; FILING DATE: 24-MAR-1998
; APPLICATION NUMBER: 60/042,376
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 2000-0456.30
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-450-515-19
Query Match 65.0%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACGCGGCGCTCG 15
Db 2 GACGCGGCGCTCG 14
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; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-538-864-14

Query Match 63.0%; Score 12.6; DB 3; Length 24;
Best Local Similarity 78.9%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGGCTCGGTCAAT 20
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Db 19 GCACGAGCGCTCGGATAT 1

RESULT 14
US-10-091-841A-35/c
; Sequence 35, Application US/10091841A
; Patent No. 6833493
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: del Val, Gregorio
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: BARLEY GENE FOR THIOREDOXIN AND
; TITLE OF INVENTION: NADP-THIOREDOXIN REDUCTASE
; FILE REFERENCE: 416272001410
; CURRENT APPLICATION NUMBER: US/10/091,841A
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/540,014
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-091-841A-35

Query Match 63.0%; Score 12.6; DB 3; Length 24;
Best Local Similarity 78.9%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGGCTCGGTCAAT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 19 GCACGAGCGCTCGGATAT 1

RESULT 15
US-09-396-196G-40648/c
; Sequence 40648, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann

; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40648
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-40648

Query Match 63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGGCTCGGTCAAT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 25 GCACGGCGGCTCGGATCAT 7

Search completed: May 8, 2006, 09:49:41
Job time : 97 secs

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